SEIR model for COVID-19 dynamics incorporating the environment and social distancing

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```julia
# To install required package for plotting
Pkg.add("Plots")
# To install package for differential equations
Pkg.add("DifferentialEquations")

# To load the package "Plots"
using Plots
# TO load the package "DifferentialEquations"
using DifferentialEquations

# Assinged model data

# Total number of population
N = S + E + IA + IS + R
# Susceptible population
S = 93000
# Asymptomatically infected population
IA = 50
# Symptamatically infected population
IS = 50
# Recovered population
R = 0
# Pathogens population
P = 500
# Exposed population
E = 1000

# Parameters used
# Birth rate of the human population
b = 0.00018
# Natural human death rate
mu = 0.00004563
# Human life expectancy (1\mu)
mu1 = 60
# Natural death rate of pathogens in the environment
mu_p = 0.01724
# Life expectancy of pathogens in the environment (1\mu_p)
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mu_p1 = 5.8
#Proportion of interaction with an infectious environment
alpha1 = 0.1
# Proportion of interaction with an infectious individual
alpha2 = 0.1
#Rate of transmission from S to E due to contact with P
beta1 = 0.00414
# Rate of transmission from S to E due to contact with IA and/or IS
beta2 = 0.0115
# Proportion of symptomatic infectious people
delta = 0.7
# Progression rate from E back to S due to the robust immune system
psi = 0.0051
#Progression rate from E to either IA or IS
w = 0.09
# Death rate due to the coronavirus
sigma = 0.0018
# Rate of recovery of the symptomatic population
gamma_S = 0.05
# Rate of recovery of the asymptomatic human population
gamma_A = 0.0714
# Rate of virus spread to the environment by symptomatic infectious
eta_S = 0.1
# Rate of virus spread to the environment by asymptomatic infectious
eta_A = 0.05

# time span from 0 to 90 days
tspan = (0., 90)
intial_Parameters = [S,E,IA,IS,R,P]
p = [alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu,mu_p]

# Here we perform 3 variations by changing the parameters alpha1 and
# alpha2 based on reproduction number,
# initially we take alpha1 = 0.1 and alpha2 = 0.1

function model_Simulation1(dxyz,initial_Parameters,p,tspan)
    alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu = p
    S,E,IA,IS,R,P = initial_Parameters
    A = (beta1*S*P/(1+alpha1*P))
    B = beta2*S*(IA+ IS)/(1+alpha2*(IA+IS))
     dxyz[1] = (b - A - B + psi * E- mu*S)
     dxyz[2] = A + B - psi * E - mu*E - w*E
     dxyz[3] = (1-delta)*w*E - (mu + sigma)*IA - gamma_S * IA
     dxyz[4] = delta * w *E - (mu + sigma)*IS - mu * R
     dxyz[5] = gamma_S*IS + gamma_A*IA - mu*R
     dxyz[6] = eta_S * IA + eta_A*IS - mu_p*P
    dxyz
end
# To solve the ODE problem
problem1 = ODEProblem(model_Simulation1,intial_Parameters,tspan,p)
solution1 = solve(problem1)
plot(solution1,title="model variation 1",xaxis="Time(Days)",
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yaxis="No.of Individuals",label=["symptomatic" "exposed"
"asymptomaticallyInfected" "symptomaticallyInfected" "Recovered"
"Pathogens"])
# To save the image in local drive
savefig("/home/shivakrishnakarnati/Project/plot.png")



# Here we change the parameters and alpha1 and alpha2

function model_Simulation2(dxyz,initial_Parameters,p,tspan)
    alpha1 = 0.05    # Changed Constant alpha1
    alpha2 = 0     # Changed Constant alpha2
    alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu = p
    S,E,IA,IS,R,P = initial_Parameters
    A = (beta1*S*P/(1+alpha1*P))
    B = beta2*S*(IA+ IS)/(1+alpha2*(IA+IS))
     dxyz[1] = (b - A - B + psi * E- mu*S)
     dxyz[2] = A + B - psi * E - mu*E - w*E
     dxyz[3] = (1-delta)*w*E - (mu + sigma)*IA - gamma_S * IA
     dxyz[4] = delta * w *E - (mu + sigma)*IS - mu * R
     dxyz[5] = gamma_S*IS + gamma_A*IA - mu*R
     dxyz[6] = eta_S * IA + eta_A*IS - mu_p*P
    dxyz
end
problem2 = ODEProblem(model_Simulation2,intial_Parameters,tspan,p)
solution2 = solve(problem2)
plot(solution2,title="Model variation 2",xaxis="Time(Days)",
yaxis="No.of Individuals",label=["symptomatic" "exposed"
"asymptomaticallyInfected" "symptomaticallyInfected"
"Recovered" "Pathogens"])
savefig("/home/shivakrishnakarnati/Project/plot.png")



#Again changing the parameters alpha1 and alpha2

function model_Simulation3(dxyz,initial_Parameters,p,tspan)
     alpha1 = 0.1   # Changed Constant alpha1
     alpha2 = 0.05    # Changed Constant alpha2
    alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu = p
    S,E,IA,IS,R,P = initial_Parameters
    A = (beta1*S*P/(1+alpha1*P))
    B = beta2*S*(IA+ IS)/(1+alpha2*(IA+IS))
     dxyz[1] = (b - A - B + psi * E- mu*S)
     dxyz[2] = A + B - psi * E - mu*E - w*E
     dxyz[3] = (1-delta)*w*E - (mu + sigma)*IA - gamma_S * IA
     dxyz[4] = delta * w *E - (mu + sigma)*IS - mu * R
     dxyz[5] = gamma_S*IS + gamma_A*IA - mu*R
     dxyz[6] = eta_S * IA + eta_A*IS - mu_p*P
    dxyz
end
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problem3 = ODEProblem(symptamatic3,intial_Parameters,tspan,p)
solution3 = solve(problem3)
plot(solution3,title="Model variation 3",xaxis="Time(Days)",
yaxis="No.of Individuals",label=["symptomatic" "exposed"
"asymptomaticallyInfected" "symptomaticallyInfected"
"Recovered" "Pathogens"])
savefig("/home/shivakrishnakarnati/Project/plot.png")
# Here we can observe that there is no much difference
#in symptamatic rate,
# while changing the constants alpha1 and alpha2


# Calculation of Basic Reproduction number
C1 = psi + mu + w
C2 = mu + sigma + gamma_S
C3 = mu + sigma + gamma_A
U = (beta2 * b * delta * w)/mu*C1*C2
V = (beta2*b*(1-delta)w)/mu*C1*C3
X = (4*beta1*b)/mu*mu_p
Y = (eta_S*delta*w)/C1*C2
Z = (eta_A*(1-delta)*w)/C1*C3
basic_reproduction= (U+V+sqrt((U+V)^2 + X*(Y*Z)))/2
println(basic_reproduction) #4.4970833312485704e-5


# Reproduction for humans
C1 = psi + mu + w
C2 = mu + sigma + gamma_S
C3 = mu + sigma + gamma_A
A = (beta2*b)/mu*C1
B = (beta1*b)/mu*mu_p*C1
humans_Reproduction = A*(((delta *w)/C2) + ((1-delta)w)/C3)
println(humans_Reproduction)  #0.006835974264236465

# Reproduction number for pathogens
pathogens_Reproduction = B*(((eta_S*delta*w)/C2) +
((eta_A*(1-delta)*w)/C3))
println(pathogens_Reproduction) #3.7489365411688278e-6


##############################################################################

#  Implemented Model based on Indian state- Telangana Data
N = 35003674 # Total population as of March 2021
S = 2354664 # Total susceptible population during
# March 2021  to May 2021
IA = 23700 # asymptotically infected
IS = 33000 # symptomatically infected
R = 0 # recovered as of May 2021
P = 41200 # assumed number of pathogens
E = 5000
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# New model parameters
# Birth rate of the human population in Telangana as of 2021
b = 0.0569
# Natural human death rate
mu = 0.18
 #Human life expectancy (1\mu)
mu1 = 60
# Natural death rate of pathogens in the environment
mu_p = 0.02
# Life expectancy of pathogens in the environment (1\mu_p)
mu_p1 = 5.4
# Proportion of interaction with an infectious environment
alpha1 = 10.5
# Proportion of interaction with an infectious individual
alpha2 = 10.5
# Rate of transmission from S to E due to contact with P
beta1 = 8.414
# Rate of transmission from S to E due to contact with IA and/or IS
beta2 = 8.515
# Proportion of symptomatic infectious people
delta = 1.7
# Progression rate from E back to S due to the robust immune system
psi = 0.51
# Progression rate from E to either IA or IS
w = 0.1
# Death rate due to the coronavirus
sigma = 0.018
# Rate of recovery of the symptomatic population
gamma_S = 3.05
# Rate of recovery of the asymptomatic human population
gamma_A = 3.714
#Rate of virus spread to the environment by symptomatic infectious
eta_S = 1.08
eta_A = 1.09      #Rate of virus spread to the environment by
# asymptomatic infectious


tspan = (0., 60)
intial_Parameters = [S,E,IA,IS,R,P]
p = [alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu,mu_p]

function model_Telangana(dxyz,initial_Parameters,p,tspan)
    alpha1,alpha2,beta1,beta2,eta_S,eta_A,b,mu = p
    S,E,IA,IS,R,P = initial_Parameters
    A = (beta1*S*P/(1+alpha1*P))
    B = beta2*S*(IA+ IS)/(1+alpha2*(IA+IS))
     dxyz[1] = (b - A - B + psi * E- mu*S)
     dxyz[2] = A + B - psi * E - mu*E - w*E
     dxyz[3] = (1-delta)*w*E - (mu + sigma)*IA - gamma_S * IA
     dxyz[4] = delta * w *E - (mu + sigma)*IS - mu * R
     dxyz[5] = gamma_S*IS + gamma_A*IA - mu*R
     dxyz[6] = eta_S * IA + eta_A*IS - mu_p*P
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```julia
        dxyz
end
problem_T = ODEProblem(model_Telangana,intial_Parameters,tspan,p)
solution_T = solve(problem_T)
plot(solution_T,title="Extended model",xaxis="Time(Days)",
yaxis="No.of Individuals",label=["symptomatic" "exposed"
"asymptomaticallyInfected" "symptomaticallyInfected"
"Recovered" "Pathogens"])
savefig("/home/shivakrishnakarnati/Project/plot.png")


# Calculation of Basic Reproduction number
C1 = psi + mu + w
C2 = mu + sigma + gamma_S
C3 = mu + sigma + gamma_A
U = (beta2 * b * delta * w)/mu*C1*C2
V = (beta2*b*(1-delta)w)/mu*C1*C3
X = (4*beta1*b)/mu*mu_p
Y = (eta_S*delta*w)/C1*C2
Z = (eta_A*(1-delta)*w)/C1*C3
basic_reproduction= (U+V+sqrt((U+V)^2 + X*(Y*Z)))/2
println(basic_reproduction) #0.5649750628274046


# Reproduction for humans
C1 = psi + mu + w
C2 = mu + sigma + gamma_S
C3 = mu + sigma + gamma_A
A = (beta2*b)/mu*C1
B = (beta1*b)/mu*mu_p*C1
humans_Reproduction = A*(((delta *w)/C2) + ((1-delta)w)/C3)
println(humans_Reproduction)  #0.07324758998441214

# Reproduction number for pathogens
pathogens_Reproduction = B*(((eta_S*delta*w)/C2) +
((eta_A*(1-delta)*w)/C3))
println(pathogens_Reproduction) #0.0015558617548055299
```